Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1, 3, 24-29, and 31-41 are pending in the application.

Claims 1, 28 and 29 are amended as follows, wherein strikeout in brackets [~~00~~] indicates deleted terminology and underling [00] indicates added terminology.

Claim 30 is newly canceled without prejudice to later prosecution.

Claims 36-41 are new.

Claims previously canceled or withdrawn are so indicated.

Listing of Claims:

1. (Three Times Amended) A method of [~~diagnosing~~] screening for higher expression level of a nucleic acid sequence encoding SEQ ID NO:3 in tumor tissue of [~~tumor in~~] a mammal, the method comprising:

(a) detecting the level of expression of [~~a~~] the nucleic acid sequence in a test sample of tumor tissue cells obtained from the mammal~~, wherein the cells are suspected of uncontrolled growth and wherein the detecting is by contacting, under high stringency conditions, nucleic acid of the test sample cells with a nucleic acid probe comprising at least 20 contiguous nucleic acid bases from DNA 58125 (SEQ ID NO:1) or its complement (SEQ ID NO:2)~~];

(b) detecting, as in step (a) the level of expression of the nucleic acid sequence in a control sample of tissue cells of the same cell type [~~that do not exhibit uncontrolled growth~~]; and

(c) comparing the expression level of the nucleic acid sequence in the test cells with the expression level in the control cells[~~, wherein a higher expression level in the test sample indicates the presence of tumor in the mammal~~] and demonstrating higher expression level in the test sample.

2. (Canceled)

3. (Original) The method of claim 1 wherein said test sample is obtained from an individual suspected to have neoplastic cell growth or proliferation.

4.-23. (Canceled)

24. (Previously added) The method of claim 3 wherein the test sample is from a human.

25. (Previously added and amended) The method of claim 1 wherein the expression level of the nucleic acid sequence in the test sample cells is at least two-fold greater than in the control cells.

26. (Previously added) The method of claim 1 wherein the test sample is from cancerous tissue.

27. (Previously added and amended) The method of claim 26 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.

28. (Previously added and twice amended) A method of [~~diagnosing~~] detecting increased copy number of a nucleic acid sequence encoding SEQ ID NO:3 in tumor tissue of [~~tumor in~~] a mammal, the method comprising:

(a) detecting the number of copies of the nucleic acid sequence in a test sample of tumor tissue cells obtained from the mammal[~~, wherein the cells are suspected of uncontrolled growth and wherein the detecting is by contacting, under high stringency conditions, nucleic acid of the test sample cells with a nucleic acid probe comprising at least 20 contiguous nucleic acid bases from DNA 58125 (SEQ ID NO:1) or its complement (SEQ ID NO:2)~~];

(b) detecting the number of copies of a nucleic acid marker sequence on the chromosome encoding the nucleic acid sequence in the test sample, which marker gene is not amplified; and

(c) comparing the copy number of the nucleic acid sequence in the test cells with the copy number of the marker sequence[~~, wherein a higher nucleic acid sequence copy number indicates the presence of tumor in the mammal~~] and demonstrating increased copy number of the nucleic acid sequence in the test sample.

29. (Previously added and twice Amended) The method of claim 28 wherein the marker sequence is [~~detected by contacting, under high stringency conditions, nucleic acid of the test sample with a nucleic acid marker sequence comprising at least 20 contiguous nucleic acid bases from a sequence, or its complement,~~] in Chromosome 16 [~~from~~] in chromosomal regions selected from the group consisting of regions P7, P55, P89, P90, P92, P93, P94, P95, P99, P154, and P208.

30. (Previously added and newly canceled)

31. (Previously added) The method of claim 28 wherein said test sample is obtained from an individual suspected to have neoplastic cell growth or proliferation.

32. (Previously added) The method of claim 31 wherein the test sample is from a human.

33. (Previously added and amended) The method of claim 26 wherein the nucleic acid sequence copy number in the test sample cells is at least two-fold greater than the copy number of unamplified marker sequences.

34. (Previously added) The method of claim 28 wherein the test sample is from cancerous tissue.

35. (Previously added and amended) The method of claim 28 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.

Please add the following new claims:

36. (New) The method of claim 1, wherein detecting is a method selected from the group consisting of high stringency nucleic acid hybridization and polymerase chain reaction (PCR)-based methods.

37. (New) The method of claim 36, wherein the detecting methods are selected from the group consisting of *in situ* hybridization, quantitative PCR, RT-PCR, and comparative genomic hybridization.

38. (New) The method of claim 1, wherein the nucleic acid sequence is amplified in the test sample cells.

39. (New) The method of claim 28, wherein detecting is a method selected from the group consisting of high stringency nucleic acid hybridization and polymerase chain reaction (PCR)-based methods.

40. (New) The method of claim 39, wherein the detecting methods are selected from the group consisting of *in situ* hybridization, quantitative PCR, RT-PCR, and comparative genomic hybridization.

41. (New) The method of claim 28, wherein the nucleic acid sequence is amplified in the test sample cells.

Clean Set of All Pending Claims

October 29, 2003

1. (Three Times Amended) A method of screening for higher expression level of a nucleic acid sequence encoding SEQ ID NO:3 in tumor tissue of a mammal, the method comprising:

(a) detecting the level of expression of the nucleic acid sequence in a test sample of tumor tissue cells obtained from the mammal;

(b) detecting, as in step (a) the level of expression of the nucleic acid sequence in a control sample of tissue cells of the same cell type; and

(c) comparing the expression level of the nucleic acid sequence in the test cells with the expression level in the control cells and demonstrating higher expression level in the test sample.

2. (Canceled)

3. (Original) The method of claim 1 wherein said test sample is obtained from an individual suspected to have neoplastic cell growth or proliferation.

4.-23. (Canceled)

24. (Previously added) The method of claim 3 wherein the test sample is from a human.

25. (Previously added and amended) The method of claim 1 wherein the expression level of the nucleic acid sequence in the test sample cells is at least two-fold greater than in the control cells.

26. (Previously added) The method of claim 1 wherein the test sample is from cancerous tissue.

27. (Previously added and amended) The method of claim 26 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell

cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.

28. (Previously added and twice amended) A method of detecting increased copy number of a nucleic acid sequence encoding SEQ ID NO:3 in tumor tissue of a mammal, the method comprising:

(a) detecting the number of copies of the nucleic acid sequence in a test sample of tumor tissue cells obtained from the mammal;

(b) detecting the number of copies of a nucleic acid marker sequence on the chromosome encoding the nucleic acid sequence in the test sample, which marker gene is not amplified; and

(c) comparing the copy number of the nucleic acid sequence in the test cells with the copy number of the marker sequence and demonstrating increased copy number of the nucleic acid sequence in the test sample.

29. (Previously added and twice Amended) The method of claim 28 wherein the marker sequence is in Chromosome 16 in chromosomal regions selected from the group consisting of regions P7, P55, P89, P90, P92, P93, P94, P95, P99, P154, and P208.

30. (Previously added and newly canceled)

31. (Previously added) The method of claim 28 wherein said test sample is obtained from an individual suspected to have neoplastic cell growth or proliferation.

32. (Previously added) The method of claim 31 wherein the test sample is from a human.

33. (Previously added and amended) The method of claim 26 wherein the nucleic acid sequence copy number in the test sample cells is at least two-fold greater than the copy number of unamplified marker sequences.

34. (Previously added) The method of claim 28 wherein the test sample is from cancerous tissue.

35. (Previously added and amended) The method of claim 28 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.

Please add the following new claims:

36. (New) The method of claim 1, wherein detecting is a method selected from the group consisting of high stringency nucleic acid hybridization and polymerase chain reaction (PCR)-based methods.

37. (New) The method of claim 36, wherein the detecting methods are selected from the group consisting of *in situ* hybridization, quantitative PCR, RT-PCR, and comparative genomic hybridization.

38. (New) The method of claim 1, wherein the nucleic acid sequence is amplified in the test sample cells.

39. (New) The method of claim 28, wherein detecting is a method selected from the group consisting of high stringency nucleic acid hybridization and polymerase chain reaction (PCR)-based methods.

40. (New) The method of claim 39, wherein the detecting methods are selected from the group consisting of *in situ* hybridization, quantitative PCR, RT-PCR, and comparative genomic hybridization.

41. (New) The method of claim 28, wherein the nucleic acid sequence is amplified in the test sample cells.